SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Pestka, Sidney

(ii) TITLE OF INVENTION: Super Proteins Including Interferons, Interleukins, et al.

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Plevy & Associates
- (B) STREET: P.O. Box 1366, 146 Route 1, North
- (C) CITY: Edison
- (D) STATE: New Jersey
- (E) COUNTRY: U.S.A.
- (F) ZIP: 08818-1366

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb storage
- (B) COMPUTER: IBM Compatible (Intel "386" CPU)
- (C) OPERATING SYSTEM: MS-DOS 5.0
- (D) SOFTWARE: WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NO.: To Be Assigned
- (B) FILING DATE: June 10, 1994
- (C) CLASSIFICATION: To Be Assigned

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NO.: 08/076,231
- (B) FILING DATE: June 11, 1993
- (C) CLASSIFICATION: 530

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Plevy, Arthur L.

(B) REGISTRATION NO.: 24,277

(C) REFERENCE/DOCKET NO.: PESTKA-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (908) 572-5858

(B) TELEFAX: (908) 572-5963

(2) INFORMATION FOR SEQ. ID. NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 1:

TGGGCTGTGA TCTGCCTC 18

(2) INFORMATION FOR SEQ. ID. NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 2:

CATGATTTCT GCTCTGACAA CC 22

(2) INFORMATION FOR SEQ. ID. NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 3:

AACCCACAGC CTGGGTAG 18

(2) INFORMATION FOR SEQ. ID. NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 4:

GCGGGCCCCA ATGGCCYTGY CCTTT 25

(2) INFORMATION FOR SEQ. ID. NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 5:

GCTCTAGAAY TCATGAAAGY GTGA 24

(2) INFORMATION FOR SEQ. ID. NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 6:

CTTGAAGGAC AGACATG 17

(2) INFORMATION FOR SEQ. ID. NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 7:

CTGTCCTCCA TGAGATG 17

(2) INFORMATION FOR SEQ. ID. NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 8:

GGTCATTCAG CTGCTGG 17

(2) INFORMATION FOR SEQ. ID. NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 9:

TCCTCCTTCA TCAGGGG 17

(2) INFORMATION FOR SEQ. ID. NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 10:

ATTAACCCTC ACTAAAG 17

(2) INFORMATION FOR SEQ. ID. NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 11:

TAATACGACT CACTATA 17

(2) INFORMATION FOR SEQ. ID. NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULAR TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO: 12:

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                                                                    ATG GCC TTG      9
                                                                    Met Ala Leu
                                                                   -23
10  TCC TTT TCT TTA CTG ATG GTC GTG CTG GTA CTC AGC TAC AAA TCC ATC TGC TCT CTG GGC   69
    Ser Phe Ser Leu Leu Met Val Val Leu Val Leu Ser Tyr Lys Ser Ile Cys Ser Leu Gly
    -20                                 -10                                  -1
70  TGT GAT CTG CCT CAG ACC CAC AGC CTG CGT AAT AGG AGG GCC TTG ATA CTC CTG GCA CAA  129
    Cys Asp Leu Pro Gln Thr His Ser Leu Arg Asn Arg Arg Ala Leu Ile Leu Leu Ala Gln
     1                                  10                                   20
130 ATG GGA AGA ATC TCT CCT TTC TCC TGC TTG AAG GAC AGA CAT GAA TTC AGA TTC CCA GAG  189
    Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp Arg His Glu Phe Arg Phe Pro Glu
                        30                                   40
190 GAG GAG TTT GAT GGC CAC CAG TTC CAG AAG ACT CAA GCC ATC TCT GTC CTC CAT GAG ATG  249
    Glu Glu Phe Asp Gly His Gln Phe Gln Lys Thr Gln Ala Ile Ser Val Leu His Glu Met
                        50                                   60
250 ATC CAG CAG ACC TTC AAT CTC TTC AGC ACA GAG GAC TCA TCT GCT GCT TGG GAA CAG AGC  309
    Ile Gln Gln Thr Phe Asn Leu Phe Ser Thr Glu Asp Ser Ser Ala Ala Trp Glu Gln Ser
                        70                                   80
310 CTC CTA GAA AAA TTT TCC ACT GAA CTT TAC CAG CAA CTG AAT GAC CTG GAA GCA TGT GTG  369
    Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val
                        90                                  100
370 ATA CAG GAG GTT GGG GTG GAA GAG ACT CCC CTG ATG AAT GAG GAC TCC ATC CTG GCT GTG  429
    Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Ile Leu Ala Val
                       110                                  120
430 AGG AAA TAC TTC CAA AGA ATC ACT CTT TAT CTA ACA GAG AAG AAA TAC AGC CCT TGT GCC  489
    Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala
                       130                                  140
490 TGG GAG GTT GTC AGA GCA GAA ATC ATG AGA TCC CTC TCG TTT TCA ACA AAC TTG CAA AAA  549
    Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Leu Ser Phe Ser Thr Asn Leu Gln Lys
                       150                                  160
550 AGA TTA AGG AGG AAG GAT TGA  570
    Arg Leu Arg Arg Lys Asp End  166
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